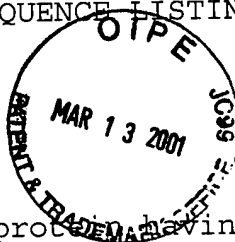


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SEQUENCE LISTING



<110> SUNTORY LIMITED

<120> Gene coding for a protein having glycosyl transferase
to aurone

<160> 6

<210> 1

<211> 1751

<212> DNA

<213> Antirrhinum majus

<220>

<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

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attttccttt taaaa atg gga aaa ctt cac att gcc tta ttt cca gtt atg 111
Met Gly Lys Leu His Ile Ala Leu Phe Pro Val Met
1 5 10
gct cat ggt cac atg atc cca atg ttg gac atg gcc aag ctc ttt acc 159
Ala His Gly His Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr
15 20 25
tca aga ggc ata caa aca aca atc att tcg act ctc gcc ttc gct gat 207
Ser Arg Gly Ile Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp
30 35 40
ccg ata aac aaa gct cgt gat tcg ggc ctc gat att gga cta agc atc 255
Pro Ile Asn Lys Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile
45 50 55 60
ctc aaa ttc cca cca gaa gga tca gga ata cca gat cac atg gtg agc 303
Leu Lys Phe Pro Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser
65 70 75

ctt gat cta gtt act gaa gat tgg ctc cca aag ttt gtt gag tca tta	351
Leu Asp Leu Val Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu	
80 85 90	
gtc tta tta caa gag cca gtt gag aag ctt atc gaa gaa cta aag ctc	399
Val Leu Leu Gln Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu	
95 100 105	
gac tgt ctc gtt tcc gac atg ttc ttg cct tgg aca gtc gat tgt gcg	447
Asp Cys Leu Val Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala	
110 115 120	
gct aag ttc ggt att ccg agg ttg gtt ttc cac gga acg agc aac ttt	495
Ala Lys Phe Gly Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe	
125 130 135 140	
gcg ttg tgt gct tcg gag caa atg aag ctt cac aag cct tat aag aat	543
Ala Leu Cys Ala Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn	
145 150 155	
gta act tct gat act gag aca ttt gtt ata ccg gat ttc ccg cat gag	591
Val Thr Ser Asp Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu	
160 165 170	
ctg aag ttt gtg agg act caa gtg gct ccg ttt cag ctt gcg gaa acg	639
Leu Lys Phe Val Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr	
175 180 185	
gag aat gga ttc tca aag ttg atg aaa cag atg acg gag tct gtt ggt	687
Glu Asn Gly Phe Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly	
190 195 200	
aga agc tac ggt gtt gtg gtt aac agt ttt tat gag ctc gag tcg act	735
Arg Ser Tyr Gly Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr	
205 210 215 220	
tat gtg gat tat tac aga gag gtt ttg ggt aga aag tct tgg aat ata	783
Tyr Val Asp Tyr Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile	
225 230 235	
ggg cct ctg ttg tta tcc aac aat ggc aat gag gaa aaa gta caa agg	831
Gly Pro Leu Leu Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg	
240 245 250	
gga aag gaa tct gcg att ggc gaa cac gaa tgc ttg gct tgg ttg aat	879
Gly Lys Glu Ser Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn	
255 260 265	

tcc aag aag cag aat tcg gtt gtt tac gtt tgt ttt gga agt atg gcg	927
Ser Lys Lys Gln Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala	
270 275 280	
act ttt act cca gcg cag ttg cgc gaa act gcg att gga ctc gag gaa	975
Thr Phe Thr Pro Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu	
285 290 295 300	
tca ggc caa gag ttc att tgg gta gtt aaa aag gcc aaa aac gaa gaa	1023
Ser Gly Gln Glu Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu	
305 310 315	
gaa gga aaa gga aaa gaa gaa tgg ctg cca gaa aat ttt gag gaa aga	1071
Glu Gly Lys Gly Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg	
320 325 330	
gtg aaa gat aga ggc ttg atc ata aga gga tgg gcg ccg caa ttg ttg	1119
Val Lys Asp Arg Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu	
335 340 345	
ata ctc gat cat cct gcg gta gga gct ttc gtg acg cat tgt gga tgg	1167
Ile Leu Asp His Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp	
350 355 360	
aat tcg acg ttg gaa gga ata tgc gcc ggt gtg cct atg gtg act tgg	1215
Asn Ser Thr Leu Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp	
365 370 375 380	
cca gtt ttc gca gag cag ttt ttc aat gag aag ttt gtg aca gag gtt	1263
Pro Val Phe Ala Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val	
385 390 395	
ttg ggg acc ggt gtt tcg gtt ggg aat aag aag tgg cta agg gca gca	1311
Leu Gly Thr Gly Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala	
400 405 410	
agt gaa ggt gtg tcg agg gag gca gtg acg aac gcg gtg cag cgt gtt	1359
Ser Glu Gly Val Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val	
415 420 425	
atg gtg gga gaa aat gcg tcg gag atg aga aag cga gcg aag tat tat	1407
Met Val Gly Glu Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr	
430 435 440	
aag gaa atg gcg agg cgg gcg gtt gag gaa ggc ggt tcg tct tat aat	1455
Lys Glu Met Ala Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn	
445 450 455 460	

ggt ttg aat gag atg ata gag gat ttg agt gtg tac cgt gct cca gaa 1503
 Gly Leu Asn Glu Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu
 465 470 475
 aaa caa gac tta aac tagattctta tagatgactt ctagtgtgac aattgtaatt 1558
 Lys Gln Asp Leu Asn
 480
 ttttgcccttt tattcaagtt tcctcattag tgttgagagc tttccctgta ttttcagaat 1618
 tgggtttgttc aattttttaca tgattttgtga tagatagctg catagtttct agctgttaac 1678
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 aaaaaaaaaaaa aaa 1751

<210> 2

<211> 481

<212> PRT

<213> Antirrhinum majus

<220>

<223> Amino acid sequence of a protein having glycosyl
 transferase to aurone

<400> 2

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 Met Ile Pro Met Leu Asp Met Ala Lys Leu Phe Thr Ser Arg Gly Ile
 20 25 30
 Gln Thr Thr Ile Ile Ser Thr Leu Ala Phe Ala Asp Pro Ile Asn Lys
 35 40 45
 Ala Arg Asp Ser Gly Leu Asp Ile Gly Leu Ser Ile Leu Lys Phe Pro
 50 55 60
 Pro Glu Gly Ser Gly Ile Pro Asp His Met Val Ser Leu Asp Leu Val
 65 70 75 80
 Thr Glu Asp Trp Leu Pro Lys Phe Val Glu Ser Leu Val Leu Leu Gln
 85 90 95
 Glu Pro Val Glu Lys Leu Ile Glu Glu Leu Lys Leu Asp Cys Leu Val
 100 105 110

Ser Asp Met Phe Leu Pro Trp Thr Val Asp Cys Ala Ala Lys Phe Gly
115 120 125
Ile Pro Arg Leu Val Phe His Gly Thr Ser Asn Phe Ala Leu Cys Ala
130 135 140
Ser Glu Gln Met Lys Leu His Lys Pro Tyr Lys Asn Val Thr Ser Asp
145 150 155 160
Thr Glu Thr Phe Val Ile Pro Asp Phe Pro His Glu Leu Lys Phe Val
165 170 175
Arg Thr Gln Val Ala Pro Phe Gln Leu Ala Glu Thr Glu Asn Gly Phe
180 185 190
Ser Lys Leu Met Lys Gln Met Thr Glu Ser Val Gly Arg Ser Tyr Gly
195 200 205
Val Val Val Asn Ser Phe Tyr Glu Leu Glu Ser Thr Tyr Val Asp Tyr
210 215 220
Tyr Arg Glu Val Leu Gly Arg Lys Ser Trp Asn Ile Gly Pro Leu Leu
225 230 235 240
Leu Ser Asn Asn Gly Asn Glu Glu Lys Val Gln Arg Gly Lys Glu Ser
245 250 255
Ala Ile Gly Glu His Glu Cys Leu Ala Trp Leu Asn Ser Lys Lys Gln
260 265 270
Asn Ser Val Val Tyr Val Cys Phe Gly Ser Met Ala Thr Phe Thr Pro
275 280 285
Ala Gln Leu Arg Glu Thr Ala Ile Gly Leu Glu Glu Ser Gly Gln Glu
290 295 300
Phe Ile Trp Val Val Lys Lys Ala Lys Asn Glu Glu Glu Gly Lys Gly
305 310 315 320
Lys Glu Glu Trp Leu Pro Glu Asn Phe Glu Glu Arg Val Lys Asp Arg
325 330 335
Gly Leu Ile Ile Arg Gly Trp Ala Pro Gln Leu Leu Ile Leu Asp His
340 345 350
Pro Ala Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu
355 360 365
Glu Gly Ile Cys Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala
370 375 380
Glu Gln Phe Phe Asn Glu Lys Phe Val Thr Glu Val Leu Gly Thr Gly
385 390 395 400
Val Ser Val Gly Asn Lys Lys Trp Leu Arg Ala Ala Ser Glu Gly Val
405 410 415

Ser Arg Glu Ala Val Thr Asn Ala Val Gln Arg Val Met Val Gly Glu
 420 425 430
 Asn Ala Ser Glu Met Arg Lys Arg Ala Lys Tyr Tyr Lys Glu Met Ala
 435 440 445
 Arg Arg Ala Val Glu Glu Gly Gly Ser Ser Tyr Asn Gly Leu Asn Glu
 450 455 460
 Met Ile Glu Asp Leu Ser Val Tyr Arg Ala Pro Glu Lys Gln Asp Leu
 465 470 475 480
 Asn

<210> 3

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400>

ataactacat atgggacaac tccac

25

<210> 4

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 4

cagaacagga tccacacgta attta

25

<210> 5

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 5

ataactacat atgggaaaac ttcac

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<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 6

gaacaggatc cacacactag aagtca

26

<210> 7

<211> 1750

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

<400> 7

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Met Ala Ile Pro Thr Val

53

1

5

caa cca cat ttt gtg ctg ctt cct ttc atg gca caa ggc cat aca aat	101
Gln Pro His Phe Val Leu Leu Pro Phe Met Ala Gln Gly His Thr Asn	
10 15 20	
ccc atg att gac atc gca cgc cta ttg gca caa cgc gga gtt ata atc	149
Pro Met Ile Asp Ile Ala Arg Leu Leu Ala Gln Arg Gly Val Ile Ile	
25 30 35	
acc att ctt act aca cac ttt aat gcc act aga ttc aag aca gtc gtt	197
Thr Ile Leu Thr Thr His Phe Asn Ala Thr Arg Phe Lys Thr Val Val	
40 45 50	
gat cgg gca gta gtg gca gca cta aag att cag gta gtt cac ctc tat	245
Asp Arg Ala Val Val Ala Ala Leu Lys Ile Gln Val Val His Leu Tyr	
55 60 65 70	
ttt cca agc tta gag gct gga cta cct gaa ggg tgt gaa gct ttc gac	293
Phe Pro Ser Leu Glu Ala Gly Leu Pro Glu Gly Cys Glu Ala Phe Asp	
75 80 85	
atg ctt cct tca atg gat ttc gca atg aaa ttc ttt gat gct acc agt	341
Met Leu Pro Ser Met Asp Phe Ala Met Lys Phe Phe Asp Ala Thr Ser	
90 95 100	
agg ctt caa cca caa gtg gaa gaa atg ctt cat gaa ctg caa ccg tca	389
Arg Leu Gln Pro Gln Val Glu Glu Met Leu His Glu Leu Gln Pro Ser	
105 110 115	
cca agt tgc ata ata tct gat atg tgt ttt cca tgg aca act aat gtt	437
Pro Ser Cys Ile Ile Ser Asp Met Cys Phe Pro Trp Thr Thr Asn Val	
120 125 130	
gca caa aaa ttc aac att cct agg ctt gtt ttt cat ggg atg tgc tgt	485
Ala Gln Lys Phe Asn Ile Pro Arg Leu Val Phe His Gly Met Cys Cys	
135 140 145 150	
ttt tct tta ttg tgc ttg cac aat ttg aga gat tgg aag gag ttg gag	533
Phe Ser Leu Leu Cys Leu His Asn Leu Arg Asp Trp Lys Glu Leu Glu	
155 160 165	
tct gat ata gaa tat ttt caa gtt cca gga tta cat gac aaa att gaa	581
Ser Asp Ile Glu Tyr Phe Gln Val Pro Gly Leu His Asp Lys Ile Glu	
170 175 180	
tta aac aaa gct cag ctt tca aat att gtt aag cca aga ggt cct gat	629
Leu Asn Lys Ala Gln Leu Ser Asn Ile Val Lys Pro Arg Gly Pro Asp	
185 190 195	

tgg aat gaa ttt gca gat caa ctg aag aaa gca gaa gaa gaa gct tat	677
Trp Asn Glu Phe Ala Asp Gln Leu Lys Lys Ala Glu Glu Glu Ala Tyr	
200 205 210	
ggg ata gta gct aat agc ttt gaa gag tta gaa cca gaa tat gtc aag	725
Gly Ile Val Ala Asn Ser Phe Glu Glu Leu Glu Pro Glu Tyr Val Lys	
215 220 225 230	
gga ttg gaa aag gca aaa ggc ttg aaa att tgg cca att ggt cct gtt	773
Gly Leu Glu Lys Ala Lys Gly Leu Lys Ile Trp Pro Ile Gly Pro Val	
235 240 245	
tct ttg tgc aac aaa gag aaa cag gac aag gct gaa aga gga aac aag	821
Ser Leu Cys Asn Lys Glu Lys Gln Asp Lys Ala Glu Arg Gly Asn Lys	
250 255 260	
gct tca att gat gaa cac cag tgt cta aaa tgg cta gat tct tgg gga	869
Ala Ser Ile Asp Glu His Gln Cys Leu Lys Trp Leu Asp Ser Trp Gly	
265 270 275	
gca aac tct gta ctc ttt gta tgt ctc ggg agc cta tcg cgc ctt cca	917
Ala Asn Ser Val Leu Phe Val Cys Leu Gly Ser Leu Ser Arg Leu Pro	
280 285 290	
acg cca caa atg ata gag ctg gga ctt ggc tta gaa tcg tcg aaa aga	965
Thr Pro Gln Met Ile Glu Leu Gly Leu Gly Leu Glu Ser Ser Lys Arg	
295 300 305 310	
ccc ttt att tgg gtt gtt aga cac aag tca gat gaa ttt aaa agt tgg	1013
Pro Phe Ile Trp Val Val Arg His Lys Ser Asp Glu Phe Lys Ser Trp	
315 320 325	
cta gtt gaa gaa aat ttt gag gaa aga gtt aaa gga caa gga ctt tta	1061
Leu Val Glu Glu Asn Phe Glu Glu Arg Val Lys Gly Gln Gly Leu Leu	
330 335 340	
atc cat ggt tgg gca cca caa gta cta ata tta tct cac act tca att	1109
Ile His Gly Trp Ala Pro Gln Val Leu Ile Leu Ser His Thr Ser Ile	
345 350 355	
gga gga ttc ttg act cat tgt gga tgg aat tcg agt gtc gaa gga ata	1157
Gly Gly Phe Leu Thr His Cys Gly Trp Asn Ser Ser Val Glu Gly Ile	
360 365 370	
tct gca ggc gtt cca atg atc act tgg cca atg ttt gct gaa caa ttc	1205
Ser Ala Gly Val Pro Met Ile Thr Trp Pro Met Phe Ala Glu Gln Phe	
375 380 385 390	

tgt aat gaa agg cta ata gtg aat gta ctg aag aca gga gta aag gct	1253
Cys Asn Glu Arg Leu Ile Val Asn Val Leu Lys Thr Gly Val Lys Ala	
395 400 405	
gga att gag aat cct gtt atg ttt gga gag gaa gaa aaa gtt gga gca	1301
Gly Ile Glu Asn Pro Val Met Phe Gly Glu Glu Glu Lys Val Gly Ala	
410 415 420	
caa gtg agc aaa gat gat att aag atg gtt att gaa aga gtc atg ggc	1349
Gln Val Ser Lys Asp Asp Ile Lys Met Val Ile Glu Arg Val Met Gly	
425 430 435	
gaa gaa gag gaa gct gaa atg aga aga aaa aga gca aaa gag tta gga	1397
Glu Glu Glu Glu Ala Glu Met Arg Arg Lys Arg Ala Lys Glu Leu Gly	
440 445 450	
gaa aag gca aag agg gct atg gag gaa ggg ggt tcc tca cac ttc aac	1445
Glu Lys Ala Lys Arg Ala Met Glu Glu Gly Gly Ser Ser His Phe Asn	
455 460 465 470	
ttg aca cag ttg att caa gat gtc act gag caa gca aat att tta aaa	1493
Leu Thr Gln Leu Ile Gln Asp Val Thr Glu Gln Ala Asn Ile Leu Lys	
475 480 485	
tcc atc taggattata aagtcgattc caagttcctt ttacgatcaa tttctaacca	1549
Ser Ile	
tctactagag atggttaacaa tccaaactgc gccttttttg cacaataatt attgttttat	1609
gttcagctag cacaaaaagt ttactattag tagaaatatt tcagctggaa ctgccgaact	1669
gctatgtaca ctgatggaac aatgtatgtc atgctattca aattaactct gagctgaaaa	1729
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<210> 8

<211> 488

<212> PRT

<213> Petunia hybrida

<220>

<223> Amino acid sequence of a protein having glycosyl
transferase to aurone

<400> 8

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		20						25					30		
Gln	Arg	Gly	Val	Ile	Ile	Thr	Ile	Leu	Thr	Thr	His	Phe	Asn	Ala	Thr
	35						40					45			
Arg	Phe	Lys	Thr	Val	Val	Asp	Arg	Ala	Val	Val	Ala	Ala	Leu	Lys	Ile
	50					55					60				
Gln	Val	Val	His	Leu	Tyr	Phe	Pro	Ser	Leu	Glu	Ala	Gly	Leu	Pro	Glu
	65				70					75					80
Gly	Cys	Glu	Ala	Phe	Asp	Met	Leu	Pro	Ser	Met	Asp	Phe	Ala	Met	Lys
				85						90				95	
Phe	Phe	Asp	Ala	Thr	Ser	Arg	Leu	Gln	Pro	Gln	Val	Glu	Glu	Met	Leu
		100						105						110	
His	Glu	Leu	Gln	Pro	Ser	Pro	Ser	Cys	Ile	Ile	Ser	Asp	Met	Cys	Phe
		115					120						125		
Pro	Trp	Thr	Thr	Asn	Val	Ala	Gln	Lys	Phe	Asn	Ile	Pro	Arg	Leu	Val
	130					135						140			
Phe	His	Gly	Met	Cys	Cys	Phe	Ser	Leu	Leu	Cys	Leu	His	Asn	Leu	Arg
	145				150					155					160
Asp	Trp	Lys	Glu	Leu	Glu	Ser	Asp	Ile	Glu	Tyr	Phe	Gln	Val	Pro	Gly
			165						170					175	
Leu	His	Asp	Lys	Ile	Glu	Leu	Asn	Lys	Ala	Gln	Leu	Ser	Asn	Ile	Val
		180						185						190	
Lys	Pro	Arg	Gly	Pro	Asp	Trp	Asn	Glu	Phe	Ala	Asp	Gln	Leu	Lys	Lys
		195					200					205			
Ala	Glu	Glu	Glu	Ala	Tyr	Gly	Ile	Val	Ala	Asn	Ser	Phe	Glu	Glu	Leu
	210					215						220			
Glu	Pro	Glu	Tyr	Val	Lys	Gly	Leu	Glu	Lys	Ala	Lys	Gly	Leu	Lys	Ile
	225				230					235					240
Trp	Pro	Ile	Gly	Pro	Val	Ser	Leu	Cys	Asn	Lys	Glu	Lys	Gln	Asp	Lys
			245						250					255	
Ala	Glu	Arg	Gly	Asn	Lys	Ala	Ser	Ile	Asp	Glu	His	Gln	Cys	Leu	Lys
		260						265					270		
Trp	Leu	Asp	Ser	Trp	Gly	Ala	Asn	Ser	Val	Leu	Phe	Val	Cys	Leu	Gly
	275						280						285		
Ser	Leu	Ser	Arg	Leu	Pro	Thr	Pro	Gln	Met	Ile	Glu	Leu	Gly	Leu	Gly
	290						295					300			

Leu Glu Ser Ser Lys Arg Pro Phe Ile Trp Val Val Arg His Lys Ser
 305 310 315 320
 Asp Glu Phe Lys Ser Trp Leu Val Glu Glu Asn Phe Glu Glu Arg Val
 325 330 335
 Lys Gly Gln Gly Leu Leu Ile His Gly Trp Ala Pro Gln Val Leu Ile
 340 345 350
 Leu Ser His Thr Ser Ile Gly Gly Phe Leu Thr His Cys Gly Trp Asn
 355 360 365
 Ser Ser Val Glu Gly Ile Ser Ala Gly Val Pro Met Ile Thr Trp Pro
 370 375 380
 Met Phe Ala Glu Gln Phe Cys Asn Glu Arg Leu Ile Val Asn Val Leu
 385 390 395 400
 Lys Thr Gly Val Lys Ala Gly Ile Glu Asn Pro Val Met Phe Gly Glu
 405 410 415
 Glu Glu Lys Val Gly Ala Gln Val Ser Lys Asp Asp Ile Lys Met Val
 420 425 430
 Ile Glu Arg Val Met Gly Glu Glu Glu Glu Ala Glu Met Arg Arg Lys
 435 440 445
 Arg Ala Lys Glu Leu Gly Glu Lys Ala Lys Arg Ala Met Glu Glu Gly
 450 455 460
 Gly Ser Ser His Phe Asn Leu Thr Gln Leu Ile Gln Asp Val Thr Glu
 465 470 475 480
 Gln Ala Asn Ile Leu Lys Ser Ile
 485

<210> 9

<211> 1669

<212> DNA

<213> Petunia hybrida

<220>

<223> Nucleotide sequence coding for a protein having
glycosyl transferase to aurone

<400> 9

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tgctaagtac tactactagt acacatcttt ctttctatca aacactttcc aaa atg	116
Met	
1	
ggt cag ctc cat ttt ttc ttc ttt ccc atg atg gct cat ggc cac atg	164
Gly Gln Leu His Phe Phe Phe Phe Pro Met Met Ala His Gly His Met	
5 10 15	
att cct aca cta gac atg gct aag ctt ttc gct tca cgt ggt gtt aag	212
Ile Pro Thr Leu Asp Met Ala Lys Leu Phe Ala Ser Arg Gly Val Lys	
20 25 30	
gcc acc ata atc act act cct ctc aat gaa tca gtt ttc tcc aaa gct	260
Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys Ala	
35 40 45	
att gaa aga aac aag cat gaa att gac atc cgt ttg atc aaa ttc caa	308
Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe Gln	
50 55 60 65	
gct gtt gaa aat ggc ttg cct gaa ggt tgt gag cgt att gat ctt atc	356
Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu Ile	
70 75 80	
cct tct gat gac aag ctt tcc aat ttt ttg aaa gct gca gct atg atg	404
Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met Met	
85 90 95	
caa gaa cca ctt gag cag ctt att gaa gaa tgt cat ccc aat tgt ctt	452
Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys Leu	
100 105 110	
gtt tct gat atg ttc ctt cct tgg act act gat act gca gcc aag ttt	500
Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys Phe	
115 120 125	
aac att cca aga ata gtt ttc cat ggt acg agt ttc ttt gca ctt tgt	548
Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu Cys	
130 135 140 145	
gta gag aat agt aac agg act aat aag cca ttc aag aac gtc tct tct	596
Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser Ser	
150 155 160	
gat tct gaa act ttt gtt gta cca aat ttg cct cac gaa atc agg cta	644
Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg Leu	
165 170 175	

act aga aca caa ttg tct ccg ttt gag caa tca ttg gaa gag aca cca	692
Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr Pro	
180 185 190	
atg tcc cga atg ata aaa gca gtt agg gaa tcg gac gcg aag agt tat	740
Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser Tyr	
195 200 205	
gga gtt atc ttc aac agc ttc tat gag ctt gaa tca gat tat gtt gaa	788
Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val Glu	
210 215 220 225	
cat tat acc aag gtt ctt ggt aga aag tct tgg gct att ggc ccg ctt	836
His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro Leu	
230 235 240	
tct ttg tgc aat agg gac att gaa gat aaa gct gaa aga ggg aag att	884
Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys Ile	
245 250 255	
tcc tct att gat aaa cat gag tgt ttg aat tgg ctt gat tca aag aaa	932
Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys Lys	
260 265 270	
cca agt tcc att gtt tat gtt tgc ttc ggg agc gta gca gat ttc act	980
Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe Thr	
275 280 285	
gca gca caa atg cgt gaa ctt gca ttg gga att gaa gca tct gga caa	1028
Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly Gln	
290 295 300 305	
gaa ttc att tgg gct gtt aga aga ggc aaa gag gaa caa gac aat gaa	1076
Glu Phe Ile Trp Ala Val Arg Arg Gly Lys Glu Glu Gln Asp Asn Glu	
310 315 320	
gag tgg ttg cct gaa gga ttc gag gaa aga acg aaa gaa aaa ggt cta	1124
Glu Trp Leu Pro Glu Gly Phe Glu Glu Arg Thr Lys Glu Lys Gly Leu	
325 330 335	
att att aga gga tgg gcg ccc caa gtg cta att ctt gat cac caa gct	1172
Ile Ile Arg Gly Trp Ala Pro Gln Val Leu Ile Leu Asp His Gln Ala	
340 345 350	
gtg gga gct ttt gtc act cat tgt ggt tgg aat tca acg ctt gaa gga	1220
Val Gly Ala Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu Gly	
355 360 365	

gta tca gca ggg gtg cct atg gtg acc tgg cct gtg ttt gca gag caa 1268
 Val Ser Ala Gly Val Pro Met Val Thr Trp Pro Val Phe Ala Glu Gln
 370 375 380 385
 ttt ttc aat gaa aag ttg gtg act gag gtt ttg aga act ggg gct ggt 1316
 Phe Phe Asn Glu Lys Leu Val Thr Glu Val Leu Arg Thr Gly Ala Gly
 390 395 400
 gtt ggt tca atg caa tgg aaa aga tca gct agc gag gga gta aaa agg 1364
 Val Gly Ser Met Gln Trp Lys Arg Ser Ala Ser Glu Gly Val Lys Arg
 405 410 415
 gaa gca ata gct aag gca ata aag aga gtc atg gtg agt gaa gaa gca 1412
 Glu Ala Ile Ala Lys Ala Ile Lys Arg Val Met Val Ser Glu Glu Ala
 420 425 430
 gag gga ttc aga aac cga gct aaa gcc tac aaa gag atg gca aaa caa 1460
 Glu Gly Phe Arg Asn Arg Ala Lys Ala Tyr Lys Glu Met Ala Lys Gln
 435 440 445
 gct att gaa gaa gga gga tct tct tac tct gga ttg act act ttg cta 1508
 Ala Ile Glu Glu Gly Gly Ser Ser Tyr Ser Gly Leu Thr Thr Leu Leu
 450 455 460 465
 caa gat ata agt aca tat agt tcc aaa agt cat taactgcaca actaaaaaaaa 1561
 Gln Asp Ile Ser Thr Tyr Ser Ser Lys Ser His
 470 475
 tgtagtggtt ttctatacaa tttttatgct tttttatgcg tgtactaatt taaacatgga 1621
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<213> Petunia hybrida

<220>

<223> Amino acid sequence of a protein having glycosyl
transferase to aurone

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 Lys Ala Thr Ile Ile Thr Thr Pro Leu Asn Glu Ser Val Phe Ser Lys
 35 40 45
 Ala Ile Glu Arg Asn Lys His Glu Ile Asp Ile Arg Leu Ile Lys Phe
 50 55 60
 Gln Ala Val Glu Asn Gly Leu Pro Glu Gly Cys Glu Arg Ile Asp Leu
 65 70 75 80
 Ile Pro Ser Asp Asp Lys Leu Ser Asn Phe Leu Lys Ala Ala Ala Met
 85 90 95
 Met Gln Glu Pro Leu Glu Gln Leu Ile Glu Glu Cys His Pro Asn Cys
 100 105 110
 Leu Val Ser Asp Met Phe Leu Pro Trp Thr Thr Asp Thr Ala Ala Lys
 115 120 125
 Phe Asn Ile Pro Arg Ile Val Phe His Gly Thr Ser Phe Phe Ala Leu
 130 135 140
 Cys Val Glu Asn Ser Asn Arg Thr Asn Lys Pro Phe Lys Asn Val Ser
 145 150 155 160
 Ser Asp Ser Glu Thr Phe Val Val Pro Asn Leu Pro His Glu Ile Arg
 165 170 175
 Leu Thr Arg Thr Gln Leu Ser Pro Phe Glu Gln Ser Leu Glu Glu Thr
 180 185 190
 Pro Met Ser Arg Met Ile Lys Ala Val Arg Glu Ser Asp Ala Lys Ser
 195 200 205
 Tyr Gly Val Ile Phe Asn Ser Phe Tyr Glu Leu Glu Ser Asp Tyr Val
 210 215 220
 Glu His Tyr Thr Lys Val Leu Gly Arg Lys Ser Trp Ala Ile Gly Pro
 225 230 235 240
 Leu Ser Leu Cys Asn Arg Asp Ile Glu Asp Lys Ala Glu Arg Gly Lys
 245 250 255
 Ile Ser Ser Ile Asp Lys His Glu Cys Leu Asn Trp Leu Asp Ser Lys
 260 265 270
 Lys Pro Ser Ser Ile Val Tyr Val Cys Phe Gly Ser Val Ala Asp Phe
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 Thr Ala Ala Gln Met Arg Glu Leu Ala Leu Gly Ile Glu Ala Ser Gly
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24

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<223> Primer

<400> 14

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